IN THE CLAIMS

1-35. (Canceled).

36. (Currently Amended) A replication-competent adenovirus vector for selective cytolysis of a target cell, comprising a first and a second adenovirus gene essential for replication, wherein said first adenovirus gene is under transcriptional control of a human carcinoembryonic antigen transcription regulatory element (CEA-TRE) and said second adenovirus gene is under transcriptional control of a cell-specific, tissue-specific or cancer-specific heterologous transcriptional regulatory element (TRE), and wherein said CEA-TRE ~~comprises~~ consists essentially of a polynucleotide sequence within about -402 to about +69 nucleotides relative to the transcriptional start site of the CEA gene and a polynucleotide sequence including nucleotides from about -14.5 to about -3.8 kilobases or from about -6.1 to about -3.8 kilobases relative to the transcriptional start site of the CEA gene.

37-42. (Canceled).

43. (Currently Amended) The adenovirus vector of Claim 36, wherein said CEA enhancer ~~comprises~~ consists essentially of a polynucleotide sequence from about -6.1 to about -3.8 kilobases relative to the transcriptional start site of the CEA gene.

44. (Currently Amended) The adenovirus vector of Claim 36, wherein said CEA enhancer ~~comprises~~ consists essentially of a polynucleotide sequence from about -14.5 to about -3.8 kilobases relative to the transcriptional start site of the CEA gene.

45. (Currently Amended) The adenovirus vector of Claim 36, wherein said CEA promoter ~~comprises~~ consists essentially of the nucleotide sequence as shown in SEQ ID NO:1.

46. (Currently Amended) The adenovirus vector of Claim 36 wherein said CEA ~~enhancer comprises~~ TRE consists essentially of a polynucleotide sequence within the region from about -13.6 to about -10.6 kilobases relative to the transcriptional start site of the CEA gene.

47. (Currently Amended) The adenovirus vector of Claim 36 wherein said ~~enhancer comprises~~ TRE consists essentially of a polynucleotide sequence from about -14.5 to about -10.6 kilobases relative to the transcriptional start site of the CEA gene.

48. (Currently Amended) The adenovirus vector of Claim 36 wherein said CEA ~~promoter~~ TRE is a sequence having at least 85% sequence identity to ~~nucleotides -402 to +69 as depicted in~~ SEQ ID NO:1, wherein said promoter component retains the ability to increase transcription of an operably linked polynucleotide.

49. (Currently Amended) The adenovirus vector of Claim 36 wherein said CEA ~~promoter~~ TRE is a sequence having at least 90% sequence identity to ~~nucleotides -402 to +69 as depicted in~~ SEQ ID NO:1, wherein said promoter component retains the ability to increase transcription of an operably linked polynucleotide.

50. (Currently Amended) The adenovirus vector of Claim 36 wherein said CEA ~~promoter~~ TRE is a sequence having at least 95% sequence identity to ~~nucleotides -402 to +69 as depicted in~~ SEQ ID NO:1, wherein said promoter component retains the ability to increase transcription of an operably linked polynucleotide.

51. (New) The adenovirus vector of Claim 36, further comprising a transgene encoding GM-CSF, operatively linked to a TRE other than a CEA-TRE.

52. (New) The adenovirus vector of Claim 36 further comprising a transgene encoding herpes simplex gene encoding thymidine kinase (HSV-tk), operatively linked to a TRE other than a CEA-TRE.